

Priority

1652

#9

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/339,159A

DATE: 06/09/2000
TIME: 17:03:39

Input Set: I339159A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Kauppinen, Markus Sakari
2 Schulein, Martin
3 Schnorr, Kirk
4 Andersen, Lene Nonboe
5 Bjornvad, Mads Eskelund
6 <120> TITLE OF INVENTION: Novel Mannanases
7 <130> FILE REFERENCE: 5440.204-US
8 <140> CURRENT APPLICATION NUMBER: US/09/339,159A
9 <141> CURRENT FILING DATE: 1999-06-24
10 <150> EARLIER APPLICATION NUMBER: 60/106,054
11 <151> EARLIER FILING DATE: 1998-10-28
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14 <150> EARLIER APPLICATION NUMBER: 60/123,543
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20 <150> EARLIER APPLICATION NUMBER: 60/123,642
21 <151> EARLIER FILING DATE: 1999-03-11
22 <160> NUMBER OF SEQ ID NOS: 34
23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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25 <211> LENGTH: 1470
26 <212> TYPE: DNA
27 <213> ORGANISM: Bacillus sp. I633
28 <400> SEQUENCE: 1

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47      ggtccttggg ctgtgacaga gtggtcttct aaaggaagtc attctttaaa agcggatatt 1140
48      caattgtcgt caaattcaca acattactta catgttattc aaaatacgtc tttacagcag 1200
49      aatagtagga tacaagctac tgttaaacat gcaaattggg gaagtgttgg taatggaatg 1260
50      actgcgcgtc tttatgtgaa aacaggacat ggttatacat ggtactctgg aagctttgtg 1320
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62      20          25          30
63      Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly
64      35          40          45
65      Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
66      50          55          60
67      Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn
68      65          70          75          80
69      Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp
70      85          90          95
71      Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu
72      100         105         110
73      Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala
74      115         120         125
75      Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu
76      130         135         140
77      Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe
78      145         150         155         160
79      Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile
80      165         170         175
81      Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala
82      180         185         190
83      Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu
84      195         200         205
85      Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met
86      210         215         220
87      Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp
88      225         230         235         240
89      Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
90      245         250         255
91      Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser
92      260         265         270
93      Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly
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99      Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly
100                      325                      330                      335
101     Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly
102                      340                      345                      350
103     Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp
104                      355                      360                      365
105     Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser
106                      370                      375                      380
107     Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln
108                      385                      390                      395                      400
109     Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val
110                      405                      410                      415
111     Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr
112                      420                      425                      430
113     Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr
114                      435                      440                      445
115     Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg
116                      450                      455                      460
117     Glu Ile Gly Val Gln Phe Gln Ser Ala Ser Asp Ser Ser Gly Gln Thr
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128     gaagggattg caaataaccg tgcataacg gtccggattg tggtatctga tgggggacaa 180
129     tggacaaaag atgacatcca tacagtaaga aaccttatct ctttagcggg agataatcat 240
130     ttggttgctg ttcctgaagt tcatgatgct accggttatg attccattgc ttcgctcaat 300
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132     attattaata ttgcgaatga atggtttggg tcgtgggaag gggatgcttg ggctgacggg 420
133     tataaacaag caatcccgcg attgcgtaac gccggtctaa accatacctt gatggtagat 480
134     gctgcggggg ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540
135     gctgaccctc aacgaaatac aatgttttcg attcatatgt atgaatatgc aggtggtaat 600
136     gcatcgcaag ttcgtactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660
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141     agcccgggaa caacaccaga gccgaccgca aatacaccgg tatcaggcaa tttgaagggt 960
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143     actaataccg gaagcagtgc aattgatttg tccaaactca cattgagata ttattataca 1080
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147 gcacatgttc agatacaagg tagatttgca aagaatgact ggagtaacta tacacagtca 1320
148 aatgactact cattcaagtc tcgttcacag ttgttgaat gggatcaggt aacagcatac 1380
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159 Lys Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala
160 35 40 45
161 Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp
162 50 55 60
163 Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His
164 65 70 75 80
165 Leu Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile
166 85 90 95
167 Ala Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala
168 100 105 110
169 Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp
170 115 120 125
171 Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala
172 130 135 140
173 Ile Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp
174 145 150 155 160
175 Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg
176 165 170 175
177 Glu Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His
178 180 185 190
179 Met Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile
180 195 200 205
181 Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly
182 210 215 220
183 His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr
184 225 230 235 240
185 Ser Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn
186 245 250 255
187 Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn
188 260 265 270
189 Asn Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu
190 275 280 285
191 Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro
192 290 295 300
193 Thr Pro Glu Pro Thr Ala Asn Thr Pro Val Ser Gly Asn Leu Lys Val
194 305 310 315 320

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196               325                      330                      335
197   Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys
198               340                      345                      350
199   Leu Thr Leu Arg Tyr Tyr Tyr Thr Val Asp Gly Gln Lys Asp Gln Thr
200               355                      360                      365
201   Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn
202               370                      375                      380
203   Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser
204               385                      390                      395                      400
205   Thr Asn Asn Ala Asp Thr Tyr Leu Glu Ile Ser Phe Thr Gly Gly Thr
206               405                      410                      415
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208               420                      425                      430
209   Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg
210               435                      440                      445
211   Ser Gln Phe Val Glu Trp Asp Gln Val Thr Ala Tyr Leu Asn Gly Val
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215 <210> SEQ ID NO 5

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217 <212> TYPE: DNA

218 <213> ORGANISM: Bacillus agaradhaerens

219 <400> SEQUENCE: 5

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222   aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
223   gcttggtata aagacaccgc ttcaacagct attcctgcc a ttgcagagca aggcgccaac 240
224   acgattcgta ttgttttatc agatggcggg caatgggaaa aagacgacat tgacaccatt 300
225   cgtgaagtca ttgagcttgc ggagcaaaat aaaatggtgg ctgtcgttga agttcatgat 360
226   gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420
227   aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480
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229   gatgccggct taacacacac cttaatggtt gatgcagcag gatgggggca atatccgcaa 600
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231   tccatccata tgtatgagta tgctggtggt gatgctaaca ctgttagatc aaatattgat 720
232   agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780
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VERIFICATION SUMMARY
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